

FIG. 1

2/21

LINKER #1 15bp SV40 ORIGIN=332bp
 GACGTCGCGG CCGCTCTAGG CCTCCAAAA AGCCTCTCA CTACTTCTGG AATAGCTCAG 60
 AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
 GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180
 ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240
 GACTTTCCAC ACCTGGTTGC TGAATAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
 GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT 360
 AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420
 GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480
 ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
 TGGGTGGACT ATTTACGGTA AACTGCCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
 AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC CCTGGCATTG TGCCAGTAC 660
 ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
 ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780
 TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840
 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900
 CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
 CATCACAGAT CTCTCACCAT GAGGGTCCCC GCTCAGCTCC TGGGGCTCCT GCTGCTCTGG 1020
 CTCCCAGGTG CACGATGTGA TGGTACCAAG GTGGAAATCA AACGTACGGT GGCTGCACCA 1080
 TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG 1140
 TGCTGCTGA ATAATTCTA TCCAGAGAG GCCAAAGTAC AGTGAAGGT GGATAACGCC 1200
 HUMAN KAPPA CONSTANT 324bp 107 AMINO ACID & STOP CODON
 CTCCAATCGG GTAACCTCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1260
 AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1320
 TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1380
 STOP
 LIGHT
 CHAIN Eco RI LINKER #4=85bp
 TGTTCGAATTC AGATCCGTTA ACGGTACCA ACTACCTAGA CTGGATTCGT GACAACATGC 1440
 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500

FIG. 2A

3/21

GTTTGCCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCTTTTCC 1560
TAATAAAATG AGGAAATTGC **BGH poly A=231bp** ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620
GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680
GCGGTGGGCT CTATGGAACC **LINKER #5=15bp** AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCTATTG 1740
ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 1800
TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860
GGCAGTACAT CAATGGGCGT **CMV PROMOTER-ENHANCER=334bp** GGATAGCGGT TTGACTCAGG GGGATTTCCA AGTCTCCACC 1920
CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980
GTAACAACCTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
TAAGCAGAGC **LINKER #6=7bp** TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG **Sal I** ACCCGTCGAC 2100
2051 2 2058 9 **LEADER=51bp** **Mlu I 2151 2 Nhe I**
ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACGCGTGT CGCTAGCACC 2160
START HEAVY CHAIN -5 -4 -3 114 115
AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 2220
GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA 2280
GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 2340
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 2400
993bp=330 AMINO ACID & STOP CODON
AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT 2460
GACAAAACCTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 2520
TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 2580
TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640
GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 2700
CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGACTIONAAG 2760
TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820
GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAGG 2880
AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 2940
TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 3000

FIG. 2B

4/21

GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 3060
AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120
STOP HEAVY CHAIN Bam HI **LINKER #7=81bp**
CTCTCCCTGT CTCCGGGTAA ATGAGGATCC GTTAACGGTT ACCAACTACC TAGACTGGAT 3180
3144 5
TCGTGACAAC ATGCGGCCGT GATATCTACG TATGATCAGC CTCGACTGTG CTTTCTAGTT 3240
3225 6
GCCAGCCATC TGTTGTTTGC CCCTCCCCCG TGCCTTCCTT GACCCTGGAA GGTGCCACTC 3300
BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
CCACTGTCTT TTCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT 3360
CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGGAA GACAATAGCA 3420
GGCATGCTGG GGATGCGGTG GGCTCTATGG AACCAGCTGG GGCTCGACAG CGCTGGATCT 3480
3456 7
CCCGATCCCC AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 3540
3490 1
AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 3600
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 3660
GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 3720
GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 3780
GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 3840
CTGACATAGT TGTGTT GGGA GCTTGGATAG CTTGGACAGC TCAGGGCTGC GATTTGCGCG 3900
3856 7 3875 6
LINKER #9=19bp **5' UNTRANSLATED DHFR=82bp**
CAAACTTGAC GGCAATCCTA GCGTGAAGGC TGGTAGGATT TTATCCCCGC TGCCATCATG 3960
3957 8
START DHFR
GTTTCGACCAT TGAAGTGCAT CGTCGCCGTG TCCCAAAATA TGGGGATTGG CAAGAACGGA 4020
GACCTACCTT GGCTCCGCT CAGGAACGAG TTCAAGTACT TCCAAAGAAT GACCACAACC 4080
TCTTCAGTGG AAGGTAAACA GAATCTGGTG ATTATGGGTA GGAAAACCTG GTTCTCCATT 4140
MOUSE DHFR=564bp=187 AMINO ACID & STOP CODON
CCTGAGAAGA ATCGACCTTT AAAGGACAGA ATTAATATAG TTCTCAGTAG AGAACTCAA 4200
GAACCACCAC GAGGAGCTCA TTTTCTTGCC AAAAGTTTGG ATGATGCCTT AAGACTTATT 4260
GAACAACCGG AATTGGCAAG TAAAGTAGAC ATGGTTTGGG TAGTCGGAGG CAGTTCTGTT 4320
TACCAGGAAG CCATGAATCA ACCAGGCCAC CTTAGACTCT TTGTGACAAG GATCATGCAG 4380
GAATTTGAAA GTGACACGTT TTTCCAGAA ATTGATTTGG GGAAATATAA ACTTCTCCCA 4440
GAATACCCAG GCGTCCTCTC TGAGGTCCAG GAGGAAAAAG GCATCAAGTA TAAGTTTGAA 4500

FIG. 2C

5/21

STOP DHFR
 GTCTACGAGA AGAAAGAC TA ACAGGAAGAT GCTTTCAAGT TCTCTGCTCC CCTCCTAAAG 4560
 4521 2
 3' UNTRANSLATED DHFR=82bp LINKER #10=10bp
 TCATGCATTT TTATAAGACC ATGGGACTTT TGCTGGCTTT AGATCAGCCT CGACTGTGCC 4620
 4603 4 4613 4
 TTCTAGTTGC CAGCCATCTG TTGTTTGGCC CTCCCCGTG CCTTCCTTGA CCCTGGAAGG 4680
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 TGCCACTCCC ACTGTCCTTT CCTAATAAAA TGAGGAAATT GCATCGCATT GTCTGAGTAG 4740
 GTGTCATTCT ATTCTGGGGG GTGGGGTGGG GCAGGACAGC AAGGGGGAGG ATTGGGAAGA 4800
 CAATAGCAGG CATGCTGGGG ATGCGGTGGG CTCTATGGAA CCAGCTGGGG CTCGAGCTAC 4860
 4844 5 LINKER #11=17bp
 TAGCTTTGCT TCTCAATTC TTATTTGCAT AATGAGAAAA AAAGGAAAAT TAATTTTAAC 4920
 ACCAATTCAG TAGTTGATTG AGCAAATGCG TTGCCAAAAA GGATGCTTTA GAGACAGTGT 4980
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 TCTCTGCACA GATAAGGACA AACATTATTC AGAGGGAGTA CCCAGAGCTG AGACTCCTAA 5040
 GCCAGTGAGT GGCACAGCAT TCTAGGGAGA AATATGCTTG TCATCACCGA AGCCTGATTG 5100
 CGTAGAGCCA CACCTTGGTA AGGGCCAATC TGCTCACACA GGATAGAGAG GGCAGGAGCC 5160
 AGGGCAGAGC ATATAAGGTG AGGTAGGATC AGTTGCTCCT CACATTTGCT TCTGACATAG 5220
 TTGTGTTGGG AGCTTGGATC GATCCTCTAT GTTGAACAA GATGGATTGC ACGCAGGTTC 5280
 5227 8 5248 9 LINKER #12=21bp START NEO
 TCCGGCCGCT TGGGTGGAGA GGCTATTCGG CTATGACTGG GCACAACAGA CAATCGGCTG 5340
 CTCTGATGCC GCCGTGTTCC GGCTGTCAGC GCAGGGGCGC CCGGTTCTTT TTGTCAAGAC 5400
 NEOMYCIN PHOSPHOTRANSFERASE
 CGACCTGTCC GGTGCCCTGA ATGAACTGCA GGACGAGGCA GCGCGGCTAT CGTGGCTGGC 5460
 795bp=264 AMINO ACIDS & STOP CODON
 CACGACGGGC GTTCCTTGCG CAGCTGTGCT CGACGTTGTC ACTGAAGCGG GAAGGGACTG 5520
 GCTGCTATTG GGCGAAGTGC CGGGGCAGGA TCTCCTGTCA TCTCACCTTG CTCCTGCCGA 5580
 GAAAGTATCC ATCATGGCTG ATGCAATGCG GCGGCTGCAT ACGCTTGATC CGGCTACCTG 5640
 CCCATTGAC CACCAAGCGA AACATCGCAT CGAGCGAGCA CGTACTCGGA TGAAGCCGG 5700
 TCTTGTCGAT CAGGATGATC TGGACGAAGA GCATCAGGGG CTCGCGCCAG CCGAACTGTT 5760
 CGCCAGGCTC AAGGCGCGCA TGCCCGACGG CGAGGATCTC GTCGTGACCC ATGGCGATGC 5820
 CTGCTTGCCG AATATCATGG TGGAAAATGG CCGCTTTTCT GGATTCATCG ACTGTGGCCG 5880
 GCTGGGTGTG GCGGACCGCT ATCAGGACAT AGCGTTGGCT ACCCGTGATA TTGCTGAAGA 5940
 GCTTGCGGC GAATGGGCTG ACCGCTTCCT CGTGCTTTAC GGTATCGCCG CTTCCCGATTG 6000

FIG. 2D

6/21

GCAGCGCATC GCCTTCTATC GCCTTCTTGA CGAGTTCTTC STOP NEO TGAGCGGGAC TCTGGGGTTC 6060
6043 4
GAAATGACCG ACCAAGCGAC GCCCAACCTG CCATCACGAG ATTTGATTTC CACCGCCGCC 6120
3' UNTRANSLATED NEO=173bp
TTCTATGAAA GGTTGGGCTT CGGAATCGTT TTCCGGGACG CCGGCTGGAT GATCCTCCAG 6180
CGCGGGGATC TCATGCTGGA GTTCTTCGCC CACCCCAACT TGTATTATGC AGCTTATAAT 6240
6216 7
GGTTACAAAT AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTTT TCACTGTCAT 6300
SV40 POLY A EARLY=133bp LINKER #13=19bp
TCTAGTTGTG GTTTGTCCAA ACTCATCAAT CTATCTTATC ATGTCTGGAT CGCGGCCGCG 6360
6349 50
ATCCCGTGA GAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC 6420
6368 9
CGCTCACAAT TCCACACAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT 6480
AATGAGTGAG CTAATCACA TTAATTGCGT TCGCTCACT GCCCGCTTTC CAGTCGGGAA 6540
ACCTGTCGTG CCAGCTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA 6600
PVC 19
TTGGGCGCTC TTCCGCTTCC TCGCTCACTG ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC 6660
GAGCGGTATC AGCTCACTCA AAGGCGGTAA TACGGTTATC CACAGAATCA GGGGATAACG 6720
CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG GAACCGTAA AAGGCCGCGT 6780
6792=BACTERIAL ORIGIN OF REPLICATION
TGCTGGCGTT TTTCCATAGG CTCCGCCCCC CTGACGAGCA TCACAAAAT CGACGCTCAA 6840
GTCAGAGGTG GCGAAACCCG ACAGGACTAT AAAGATACCA GGC GTTTCCC CCTGGAAGCT 6900
CCCTCGTGCG CTCTCCTGTT CCGACCCTGC CGCTTACCGG ATACCTGTCC GCCTTTCTCC 6960
CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG 7020
TCGTTGCTC CAAGCTGGGC TGTGTGCACG AACCCCCCGT TCAGCCCGAC CGCTGCGCCT 7080
TATCCGGTAA CTATCGTCTT GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG 7140
CAGCCACTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA 7200
AGTGGTGGCC TAACTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA 7260
AGCCAGTTAC CTTGGAAGAA AGAGTTGGTA GCTCTTGATC CGGCAACAA ACCACCGCTG 7320
GTAGCGGTGG TTTTTTTGTT TGCAAGCAGC AGATTACGCG CAGAAAAAA GGATCTCAAG 7380
AAGATCCTTT GATCTTTTCT ACGGGGTCTG ACGCTCAGTG GAACGAAAAC TCACGTAAAG 7440
GGATTTTGGT CATGAGATTA TCAAAAAGGA TCTTACCTA GATCCTTTTA AATTAAAAAT 7500

FIG. 2E

7/21

GAAGTTTTAA ATCAATCTAA AGTATATATG AGTAAACTTG GTCTGACAGT TACCAATGCT 7560
7550
TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTTTCG TTCATCCATA GTTGCCTGAC 7620
TCCCCGTCGT GTAGATAACT ACGATACGGG AGGGCTTACC ATCTGGCCCC AGTGCTGCAA 7680
TGATACCGCG AGACCCACGC TCACCGGCTC CAGATTTATC AGCAATAAAC CAGCCAGCCG 7740
BETA LACTAMASE=861bp
GAAGGGCCGA GCGCAGAAGT GGTCTTGCAA CTTTATCCGC CTCCATCCAG TCTATTAATT 7800
286 AMINO ACID & STOP CODON
GTTGCCGGGA AGCTAGAGTA AGTAGTTCGC CAGTTAATAG TTTGCGCAAC GTTGTTGCCA 7860
TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT GGCTTCATTC AGCTCCGGTT 7920
CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAGCG GTTAGCTCCT 7980
TCGGTCCTCC GATCGTTGTC AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG 8040
CAGCACTGCA TAATTCTCTT ACTGTCATGC CATCCGTAAG ATGCTTTTCT GTGACTGGTG 8100
AGTACTCAAC CAAGTCATTC TGAGAATAGT GTATGCGGCG ACCGAGTTGC TCTTGCCCGG 8160
CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA 8220
AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTTGATGT 8280
AACCCACTCG TGCACCCAAC TGATCTTCAG CATCTTTTAC TTTCACCAGC GTTTCTGGGT 8340
GAGCAAAAAC AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT 8400
START BETA LACTAMASE
GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
8410
TGAGCGGATA CATATTTGAA TGTATTTAGA AAAATAAACA AATAGGGGTT CCGCGCACAT 8520
TTCCCCGAAA AGTGCCACCT

FIG. 2F

8/21

LINKER #1=15bp
GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
15 6

AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120

SV40 ORIGIN=332bp
GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GGCAGGATGG GCGGAGTTAG GGGCGGGACT 180
ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240
GACTTTCCAC ACCTGGTTGC TGAATAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300

LINKER #2=13bp
GGGGAGCCTG GGGACTTTCC ACACCTAAC TGACACACAT TCCACAGAAAT TAATTCCCCT 360
347 8

AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420
GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480
ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540

CVM PROMOTER-ENHANCER=567bp
TGGGTGGACT ATTTACGGTA AACTGCCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGCCAGTAC 660
ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780
TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840
GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900

LINKER #3=7bp
CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
927 8 934 5

Bgl 2 START LIGHT CHAIN NATURAL LEADER=66bp
CATCACAGAT CTCTCACTAT GGATTTTCAG GTGCAGATTA TCAGCTTCCT GCTAATCAGT 1020
978 9

GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT 1080
1044 5+1

GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAGGGCCA GCTGAAGTGT AAGTTACATC 1140
CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCCT GGATTTATGC CACATCCAAC 1200

LIGHT CHAIN VARIABLE REGION 318bp 106 AMINO ACID
CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTACTCTCTC 1260
ACCATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT 1320

BsiWI
AACCACCCA CGTTCGGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCACCA 1380
1362 3

TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACTGC CTCTGTTGTG 1440
TGCTGCTGA ATAATTCTA TCCAGAGAG GCCAAAGTAC AGTGGAAGGT GGATAACGCC 1500

FIG. 3A

9/21

HUMAN KAPPA CONSTANT=324bp=107 AMINO ACID & STOP CODON
 CTCCAATCGG GTAACCTCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1560
 AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1620
 TCGGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1680
STOP
LIGHT CHAIN Eco RI **LINKER #4=81bp**
 TGTGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC 1740
 1646 7 1771 2
 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1800
 GTTTGCCCTT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCAC TGTCCTTTCC 1860
 TAATAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1920
BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1980
LINKER #5=15bp
 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 2040
 2002 3 2017 8
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 2100
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 2160
CMV PROMOTER-ENHANCER=334bp
 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCAC AGTCTCCACC 2220
 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAATGTC 2280
 GTAACAATC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2340
LINKER #6=7bp Sal I
 TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCCGAC 2400
 2351 2 2358 9
START
HEAVY CHAIN **SYNTHETIC & NATURAL LEADER** Mlu I 2457 8
 ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACCGGTGT CTTGTCCAG 2460
 2401 -5 -4 -3 -2 -1 +1
 GTACAATGC AGCAGCCTGG GGCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATGTCC 2520
 TGCAAGGCTT CTGGCTACAC ATTTACCACT TACAATATGC ACTGGGTAAA ACAGACACCT 2580
HEAVY CHAIN VARIABLE=363bp=121 AMINO ACID
 GGTCGGGGCC TGGAAATGGAT TGGAGCTATT TATCCCGGAA ATGGTGATAC TTCCTACAAT 2640
 CAGAAGTTCA AAGGCAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 2700
 CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ACTGTGCAAG ATCGACTTAC 2760
 TACGGCGGTG ACTGGTACTT CAATGTCTGG GCGGCAGGGA CCACGGTCAC CGTCTCTGCA 2820
Nhe I
 GCTAGCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCTT CCTCCAAGAG CACCTCTGGG 2880
 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 2940
HUMAN GAMMA 1 CONSTANT=993bp
 TGGAATCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA 3000

FIG. 3B

00021060-002997

10/21

330 AMINO ACID & STOP CODON
GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 3060
TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGCAGAGCCC 3120
AAATCTTGTG ACAAACCTCA CACATGCCCC CCGTGCCCAG CACCTGAACT CCTGGGGGGA 3180
CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT 3240
GAGGTCACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG 3300
TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC 3360
AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG 3420
GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC 3480
AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCATC CCGGGATGAG 3540
CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG GCTTCTATCC CAGCGACATC 3600
GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAAC ACAAGACCAC GCCTCCCGTG 3660
CTGGACTCCG ACGGCTCCTT CTTCTCTAC AGCAAGCTCA CCGTGGACAA GAGCAGGTGG 3720
CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG 3780
STOP HEAVY CHAIN Bam HI LINKER #7=81bp
CAGAAGAGCC TCTCCCTGTC TCCGGGTAAA TGAGGATCCG TTAACGGTTA CCAACTACCT 3840
3813 4
AGACTGGATT CGTGACAACA TGCGGCCGTG ATATCTACGT ATGATCAGCC TCGACTGTGC 3900
3894 5
CTTCTAGTTG CCAGCCATCT GTTGTITGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAA 3960
GTGCCACTCC CACTGTCCTT TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA 4020
BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
GGTGTCAATC TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGGAAG 4080
ACAATAGCAG GCATGCTGGG GATGCGGTGG GCTCTATGGA ACCAGCTGGG GCTCGACAGC 4140
4125 6
GCTGGATCTC CCGATCCCCA GCTTTGCTTC TCAATTTCTT ATTTGCATAA TGAGAAAAAA 4200
AGGAAAATTA ATTTAACAC CAATTCAGTA GTTGATTGAG CAAATGCGTT GCCAAAAAGG 4260
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
ATGCTTTAGA GACAGTGGTC TCTGCACAGA TAAGGACAAA CATTATTGAG AGGGAGTACC 4320
CAGAGCTGAG ACTCCTAAGC CAGTGAGTGG CACAGCATTC TAGGGAGAAA TATGCTTGTC 4380
ATCACCGAAG CCTGATTCCG TAGAGCCACA CCTTGGTAAG GGCCAATCTG CTCACACAGG 4440
ATAGAGAGGG CAGGAGCCAG GGCAGAGCAT ATAAGGTGAG GTAGGATCAG TTGCTCCTCA 4500

FIG. 3C

11/21

CATTGCTTC TGACATAGTT LINKER #9=19bp 5' UNTRANSLATED DHFR=82bp 4560
 GTGTTGGGAG CTGGGATAGC TTGGACAGCT CAGGGCTGCG 4525 6 4544 5
 ATTCGCGCC AAACCTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATTT TATCCCCGCT 4620
START DHFR
 GCCATCATGG TTCGACCATT GAACTGCATC GTCGCCGTGT CCCAAATAT GGGGATTGGC 4680
 4626 7
 AAGAACGGAG ACCTACCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740
 ACCACAACCT CTTCACTGGA AGGTAAACAG AATCTGGTGA TTATGGGTAG GAAAACCTGG 4800
DHFR=564bp=187 AMINO ACID & STOP CODON
 TTCTCCATTC CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860
 GAACTCAAAG AACCACCACG AGGAGCTCAT TTTCTTGCCA AAAGTTTGGG TGATGCCTTA 4920
 AGACTTATTG AACAACCGGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980
 AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040
 ATCATGCAGG AATTTGAAAG TGACACGTTT TTCCAGAAA TTGATTTGGG GAAATATAAA 5100
 CTTCTCCCAG AATACCCAGG CGTCCTCTCT GAGGTCCAGG AGGAAAAAGG CATCAAGTAT 5160
STOP DHFR 3' UNTRANSLATED DHFR=82bp
 AAGTTTGAAG TCTACGAGAA GAAAGACTAA CAGGAAGATG CTTTCAAGTT CTCTGCTCCC 5220
 5140 1 5272 3
 CTCCTAAAGC TATGCATTTT TATAAGACCA TGGGACTTTT GCTGGCTTTA LINKER #10
 =10bp GATCAGCCTC 5280
 GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC TCCCCCGTGC CTTCTTGAC 5340
BOVINE GROWTH HORMONE POLYADENYLATION=231bp
 CCTGGAAGGT GCCACTCCCA CTGTCTTTT CTAATAAAAT GAGGAAATTG CATCGCATTTG 5400
 TCTGAGTAGG TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460
LINKER #11
 TTGGAAGAC AATAGCAGGC ATGCTGGGGA TCGGTGGGC TCTATGGAAC CAGCTGGGGC 5520
 5513 4
 =17bp TCGAGCTACT AGCTTTGCTT CTCAATTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 5580
 5530 1
 AATTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 5640
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 AGACAGTGTT CTCTGCACAG ATAAGGACAA CTAGGGAGAA ATATGCTTGT CATCACCAGG 5700
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCAGG 5760
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCTC ACATTTGCTT 5880
LINKER #12=21bp START NEO
 CTGACATAGT TGTGTTGGGA GCTTGGATCG ATCTCTATG GTTGAACAAG ATGGATTGCA 5940
 5896 7 5917 8
 CGCAGGTTCT CCGGCCGCTT GGGTGGAGAG GCTATTCGSC TATGACTGGG CACAACAGAC 6000

FIG. 3D

13/21

GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC 7560
 CTGGAAGCTC CCTCGTGCGC TCTCCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG 7620
 CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT 7680
 CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC 7740
 GCTGCGCCTT ATCCGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC 7800
 CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860
 AGTTCTTGAA GTGGTGGCCT AACTACGGCT AACTAGAAG GACAGTATTT GGTATCTGCG 7920
 CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA 7980
 CCACCGCTGG TAGCGGTGGT TTTTTTGTTC GCAAGCAGCA GATTACGCGC AGAAAAAAG 8040
 GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT 8100
 CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTACCTAG ATCCTTTTAA 8160
 ATTAAAAATG AAGTTTTTAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT STOP 8220
BETA LACTAMASE
 ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG 8280
 TTGCCTGACT CCCCCTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA 8340
 GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC 8400
 BETA LACTAMASE=861bp=286 AMINO ACID & STOP CODON
 AGCCAGCCGG AAGGGCCGAG CGCAGAAAGT GTCCTGCAAC TTTATCCGCC TCCATCCAGT 8460
 CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCCGC AGTTAATAGT TTGCGCAACG 8520
 TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA 8580
 GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8640
 TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAAGT TTATCACTCA 8700
 TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG 8760
 TGA CTGGTGA G TACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT 8820
 CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA 8880
 TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940
 GGTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG 9000
 TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC 9060
 GGAAATGTTG AATACTCAT START BETA LACTAMASE CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120
 ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC 9180
 CGCGCACATT TCCCCGAAAA GTGCCACCT

FIG. 3F

[illegible]

LEADER

FRAME 1	Met	Asp	Phe	Gln	Val	Gln	Ile	Ile	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser	Val		
	ATG	GAT	TTT	CAG	GTG	CAG	ATT	ATC	AGC	TTC	CTG	CTA	ATC	AGT	GCT	TCA	GTC		
			987			996			1005			1014			1023				
-5	Ile	Met	Ser	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile	Leu	Ser	Ala	Ser
	ATA	ATG	TCC	AGA	GGA	CAA	ATT	GTT	CTC	TCC	CAG	TCT	CCA	GCA	ATC	CTG	TCT	GCA	TCT
		1038				1047			1056			1065			1074			1083	
					20			23	24		CDR1		27	29	30			34	
	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Ile	His
	CCA	GGG	GAG	AAG	GTC	ACA	ATG	ACT	TGC	AGG	GCC	AGC	TCA	AGT	GTA	AGT	TAC	ATC	CAC
		1095				1104			1113			1122			1131			1140	
35		FR2				40				45				49	50		CDR2		
	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn
	TGG	TTC	CAG	CAG	AAG	CCA	GGA	TCC	TCC	CCC	AAA	CCC	TGG	ATT	TAT	GCC	ACA	TCC	AAC
		1152				1161			1170			1179			1188			1197	
55	56	57				60		FR3		65						70			
	Leu	Ala	Ser	Gly	Val	Pro	Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser
	CTG	GCT	TCT	GGA	GTC	CCT	GTT	CGC	TTC	AGT	GGC	AGT	GGG	TCT	GGG	ACT	TCT	TAC	TCT
		1209				1218			1227			1236			1245			1254	
		75						80					85			88	89	90	
	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
	CTC	ACC	ATC	AGC	AGA	GTG	GAG	GCT	GAA	GAT	GCT	GCC	ACT	TAT	TAC	TGC	CAG	CAG	TGG
		1266				1275			1284			1293			1302			1311	
			CDR3	95		97	98		100	FR4			105		107				
	Thr	Ser	Asn	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys			
	ACT	AGT	AAC	CCA	CCC	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAA	ATC	AAA			
		1323				1332			1341			1350			1359				

FIG. 4

15/21

LEADER

-19					-15					-10					-5				
FRAME 1	Met	Gly	Trp	Ser	Leu	Ile	Leu	Leu	Phe	Leu	Val	Ala	Val	Ala	Thr	Arg	Val		
	ATG	GGT	TGG	AGC	CTC	ATC	TTG	CTC	TTC	CTT	GTC	GCT	GTT	GCT	ACG	CGT	GTC		
					2409			2418		2427		2436			2445				
-1	+1				FR1					10					15				
Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys	Ala	Gly	Ala	Ser	
CTG	TCC	CAG	GTA	CAA	CTG	CAG	CAG	CCT	GGG	GCT	GAG	CTG	GTG	AAG	CCT	GGG	GCC	TCA	
		2460			2469			2478		2487				2496	GCT		2505		
		20						25				30	31	CDR1		35	36		
Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Asn	Met	His	Trp	
GTG	AAG	ATG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACA	TTT	ACC	AGT	TAC	AAT	ATG	CAC	TGG	
		2517			2526			2536		2544			2553			2562			
				40	FR2			45				49	50		52	52A	53	54	
Val	Lys	Gln	Thr	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	
GTA	AAA	CAG	ACA	CCT	GGT	CGG	GGC	CTG	GAA	TGG	ATT	GGA	GCT	ATT	TAT	CCC	CGA	AAT	
		2574			2583			2592		2601			2610			2619			
55					CDR2	60				65	66	FR3			70				
Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	
GGT	GAT	ACT	TCC	TAC	AAT	CAG	AAG	TTC	AAA	GGC	AAG	GCC	ACA	TTG	ACT	GCA	GAC	AAA	
		2631			2640			2649		2658		2667			2676				
		75				80		82	82A	82B	82C	83		85					
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	
TCC	TCC	AGC	ACA	GCC	TAC	ATG	CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	TCT	GCG	GTC	
		2688			2697			2706		2715		2724			2733				
90					94	95			CDR3		100	100A	100B	100C	100D	101	102	103	
Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Tyr	Tyr	Gly	Gly	Asp	Trp	Tyr	Phe	Asn	Val	Trp	Gly	
TAT	TAC	TGT	GCA	AGA	TCG	ACT	TAC	TAC	GGC	GGT	GAC	TGG	TAC	TTC	AAT	GTC	TGG	GGC	
		2745			2754			2763		2772		2781			2790				
105	FR4				110			113											
Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ala											
GCA	GGG	ACC	ACG	GTC	ACC	GTC	TCT	GCA											
		2802			2811			2820											

FIG. 5

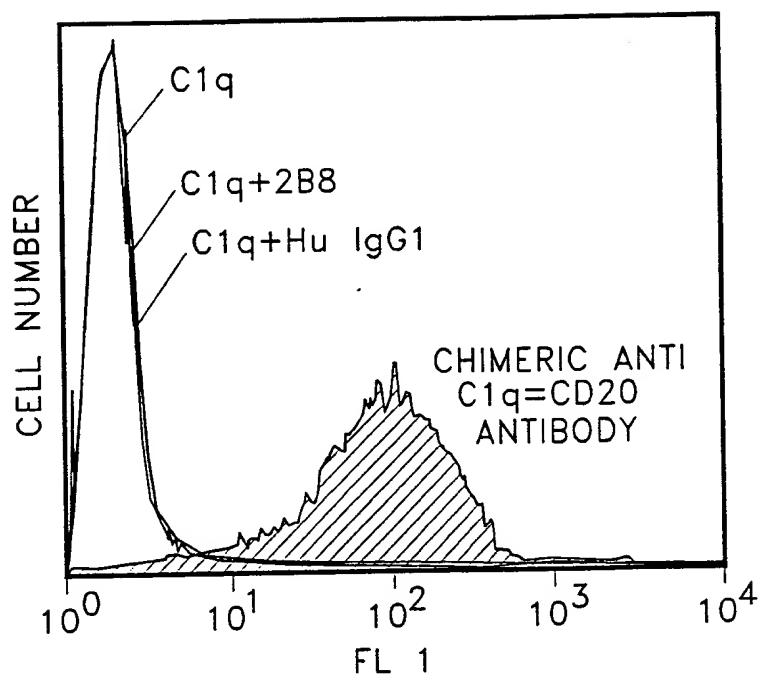


FIG. 6

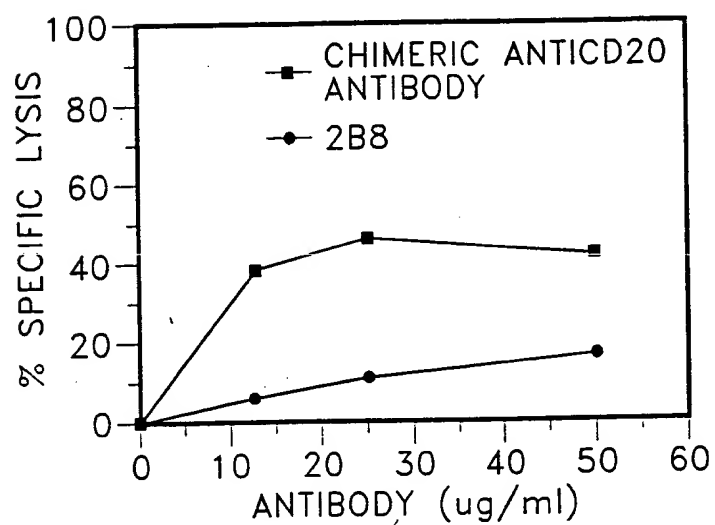
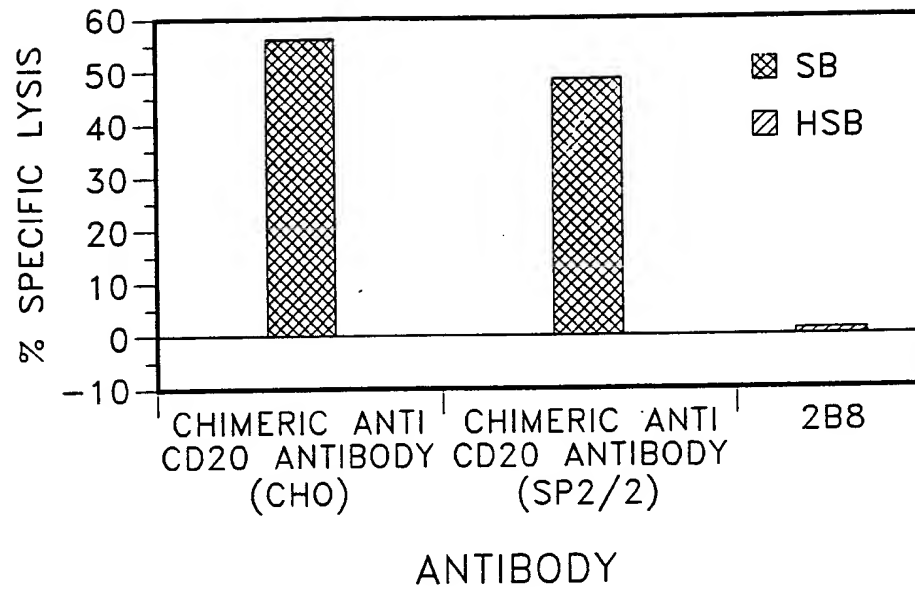
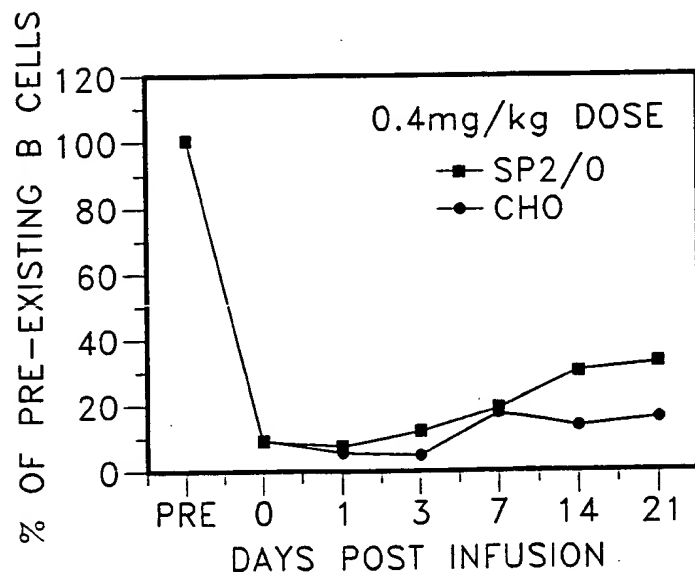
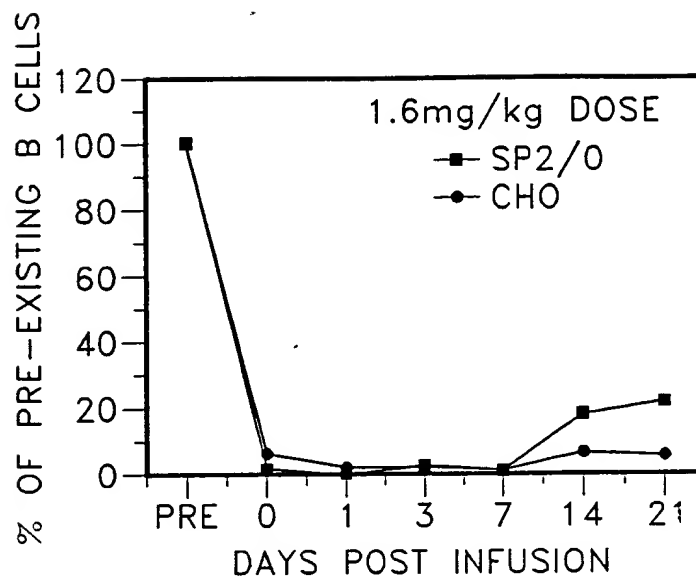
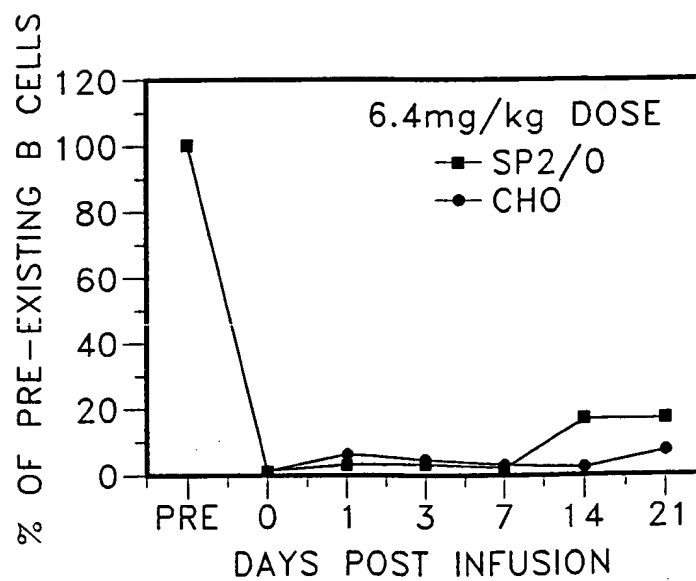
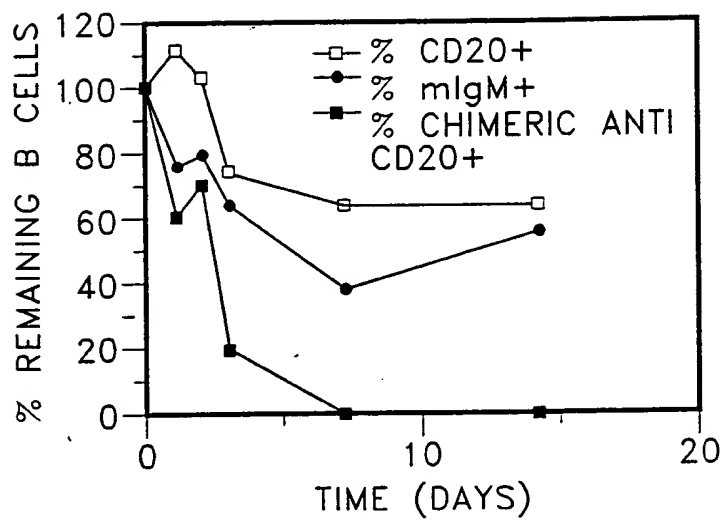
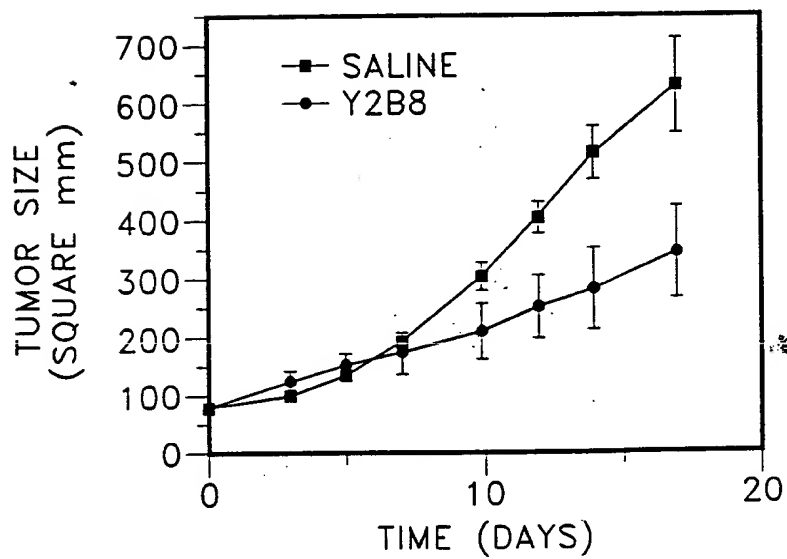
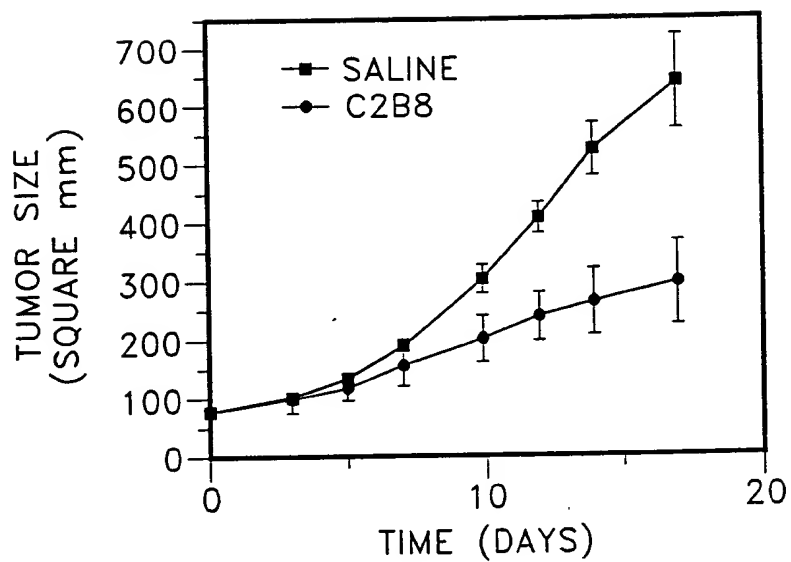
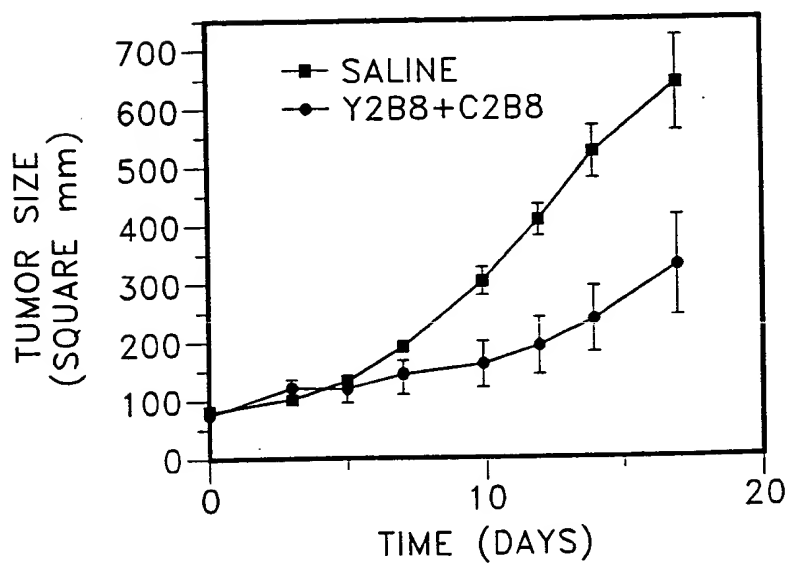


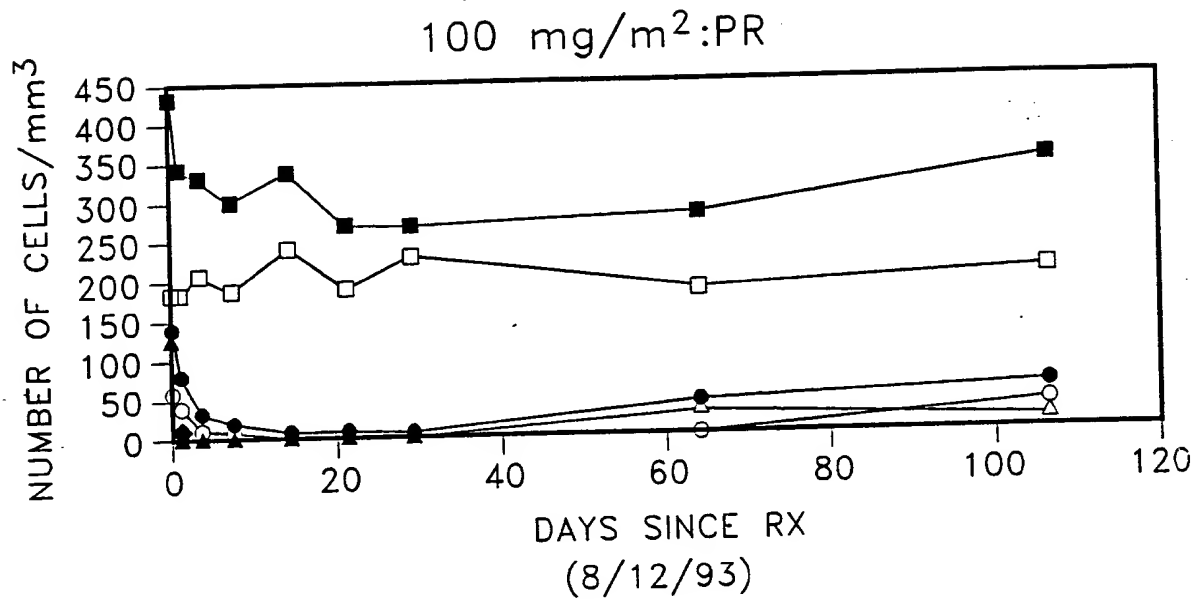
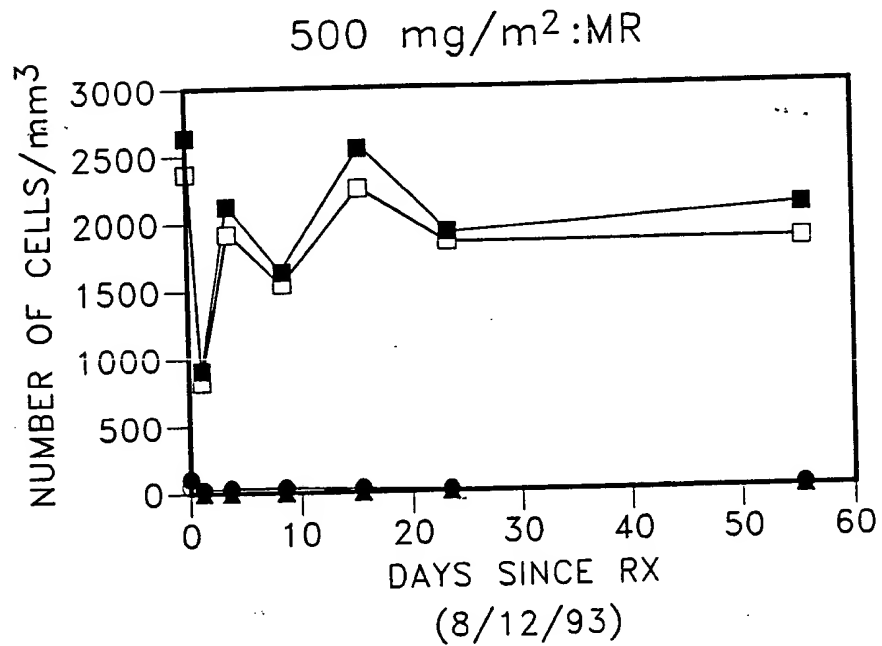
FIG. 7

*FIG. 8**FIG. 9A*

*FIG. 9B**FIG. 9C*

*FIG. 10**FIG. 11*

*FIG. 12**FIG. 13*

*FIG. 14A**FIG. 14B*